ELSEVIER

Discrete Applied Mathematics 71 (1996) 367–368

DISCRETE APPLIED MATHEMATICS

Author Index

Volume 71 (1996)

Akkiraju, N. and H. Edelsbrunner, Triangulating the surface of a molecule	(1–3)	5– 22
Atkins, J.E. and M. Middendorf, On Physical Mapping and the consecutive ones property for sparse matrices	(1–3)	23– 40
Bafna, V., B. Narayanan and R. Ravi, Nonoverlapping local alignments (weighted independent sets of axis-parallel rectangles)	(1–3)	41– 53
Bodlaender, H.L. and B. de Fluiter, On intervalizing k-colored graphs for DNA physical mapping	(1–3)	55– 77
Boneh, D., C. Dunworth, R.J. Lipton and J. Sgall, On the computational power of DNA	(1–3)	79– 94
Chen, T. and S.S. Skiena, Sorting with fixed-length reversals	(1–3)	269–295
De Fluiter, B., see H.L. Bodlaender	(1–3)	55– 77
Dress, A., D. Huson and V. Moulton, Analyzing and visualizing sequence and distance data using SPLITSTREE	(1–3)	95–109
Dunworth, C., see D. Boneh	(1–3)	79– 94
Edelsbrunner, H., see N. Akkiraju	(1–3)	5– 22
Goldberg, L.A., P.W. Goldberg, C.A. Phillips, E. Sweedyk and T. Warnow, Minimizing phylogenetic number to find good evolutionary trees	(1–3)	111–136
Goldberg, P.W., see L.A. Goldberg	(1–3)	111–136
Hannenhalli, S., Polynomial-time algorithm for computing translocation distance between genomes	(1–3)	137–151
He, B., see Z. Zhang	(1–3)	337–365
Hein, J., T. Jiang, L. Wang and K. Zhang, On the complexity of comparing evolutionary trees	(1–3)	153–169
Huson, D., see A. Dress	(1–3)	95–109
Jiang, T., see J. Hein	(1–3)	153–169
Kandel, D., Y. Matias, R. Unger and P. Winkler, Shuffling biological sequences	(1–3)	171–185
Lipton, R.J., see D. Boneh	(1–3)	79– 94
Mastronarde, D.N., see T.D. Schneider	(1–3)	259–268
Matias, Y., see D. Kandel	(1–3)	171–185
Middendorf, M., see J.E. Atkins	(1–3)	23– 40
Miller, W., see Z. Zhang	(1–3)	337–365
Moulton, V., see A. Dress	(1–3)	95–109
Nadeau, J.H., see D. Sankoff	(1–3)	247–257
Narayanan, B., see V. Bafna	(1–3)	41– 53
Paterson, M. and T. Przytycka, On the complexity of string folding	(1–3)	217–230
Pearson, W.R., G. Robins, D.E. Wrege and T. Zhang, On the primer selection problem in polymerase chain reaction experiments	(1–3)	231–246

Elsevier Science B.V.

Phillips, C. and T.J. Warnow, The asymmetric median tree – A new model for building consensus tress (1–3) 311–335
Phillips, C.A., see L.A. Goldberg (1–3) 111–136
Przytycka, T., see M. Paterson (1–3) 217–230
Ravi, R., see V. Bafna (1–3) 41– 53
Robins, G. see W.R. Pearson (1–3) 231–246
Sankoff, D. and J.H. Nadeau, Conserved synteny as a measure of genomic distance (1–3) 247–257
Schneider, T.D. and D.N. Mastronarde, Fast multiple alignment of ungapped DNA sequences using information theory and a relaxation method (1–3) 259–268
Sgall, J., see D. Boneh (1–3) 79– 94
Skiena, S.S., see T. Chen (1–3) 269–295
Smith, J.M.-G. and B. Toppur, Euclidean Steiner minimal trees, minimum energy configurations, and the embedding problem of weighted graphs in E^3 (1–3) 187–215
Sweedyk, E., see L.A. Goldberg (1–3) 111–136
Toppur, B., see J.M.-G. Smith (1–3) 187–215
Unger, R., see D. Kandel (1–3) 171–185
Vingron, M. and M.S. Waterman, Alignment networks and electrical networks (1–3) 297–309
Wang, L., see J. Hein (1–3) 153–169
Warnow, T., see L.A. Goldberg (1–3) 111–136
Warnow, T.J., see C. Phillips (1–3) 311–335
Waterman, M.S., see M. Vingron (1–3) 297–309
Winkler, P., see D. Kandel (1–3) 171–185
Wrege, D.E., see W.R. Pearson (1–3) 231–246
Zhang, K., see J. Hein (1–3) 153–169
Zhang, T., see W.R. Pearson (1–3) 231–246
Zhang, Z., B. He and W. Miller, Local multiple alignment via subgraph enumeration (1–3) 337–365